

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 05:54:17 ; Search time 70 Seconds

(without alignments)
1087.611 Million cell updates/sec

Title: US-09-817-198C-2

Perfect score: 1105

Sequence: 1 MAKQYDVLFRLLIGDSGVG.....LLEEKGKPGPANSSKTCWC 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1595201 seqs, 359116952 residues

Total number of hits satisfying chosen parameters: 1595201

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1105	100.0	212	15	US-10-363-616-319
3	1105	100.0	401	9	US-09-764-868-701
4	1092	98.8	218	9	US-09-817-198A-5
5	1077	97.5	212	9	US-09-817-198A-4
6	832	75.3	188	9	US-09-764-868-1120
7	573	51.9	208	16	US-10-408-765A-2929
8	559	50.6	224	14	US-10-369-493-4997
9	545	49.3	213	15	US-10-276-774-2286
10	540	48.9	221	15	US-10-264-049-2465
11	532	48.1	246	9	US-09-925-302-534
12	532	48.1	246	10	US-09-925-302-534
13	530.5	48.0	218	9	US-09-925-300-1571

14	528.5	47.8	207	9	US-09-794-257-8	Sequence 8, Appli
15	528.5	47.8	207	14	US-10-170-385-373	Sequence 373, App
16	528.5	47.8	207	14	US-10-400-991-65	Sequence 65, Appl
17	526.5	47.6	200	16	US-10-408-765A-1301	Sequence 1301, Ap
18	523	47.3	206	14	US-10-128-714-8600	Sequence 3241, Ap
19	523	47.3	206	14	US-10-128-714-8600	Sequence 8600, Ap
20	518	46.9	214	17	US-10-425-115-357716	Sequence 357716,
21	518	46.9	215	16	US-10-437-963-182164	Sequence 182164,
22	518	46.9	251	15	US-10-425-114-65760	Sequence 65760, A
23	517	46.8	214	16	US-10-767-701-44111	Sequence 44111, A
24	514.5	46.6	215	16	US-10-437-963-115183	Sequence 115183,
25	514	46.5	201	14	US-10-179-766-6	Sequence 6, Appli
26	514	46.5	201	14	US-10-369-493-5076	Sequence 5076, Ap
27	514	46.5	214	17	US-10-425-115-204527	Sequence 204527,
28	514	46.5	215	17	US-10-425-114-73047	Sequence 73047, A
29	513.5	46.5	215	17	US-10-425-115-361648	Sequence 361648,
30	513.5	46.5	223	15	US-10-425-114-66036	Sequence 66036, A
31	513.5	46.5	248	15	US-10-437-963-182163	Sequence 182163,
32	512.5	46.4	214	16	US-10-425-115-204526	Sequence 204526,
33	512.5	46.4	215	17	US-10-425-115-204529	Sequence 204529,
34	512.5	46.4	215	16	US-10-767-701-42756	Sequence 42756, A
35	512.5	46.4	216	15	US-10-425-114-65920	Sequence 65920, A
36	512.5	46.4	217	15	US-10-425-114-67764	Sequence 67764, A
37	512.5	46.4	217	15	US-10-425-114-70050	Sequence 70050, A
38	512.5	46.4	217	15	US-10-425-114-72771	Sequence 72771, A
39	512.5	46.4	217	15	US-09-822-860-5	Sequence 5, Appli
40	512	46.3	190	9	US-10-424-599-170355	Sequence 170355,
41	511.5	46.3	214	15	US-10-767-701-42002	Sequence 42002, A
42	511.5	46.3	214	16	US-10-424-599-201556	Sequence 201556,
43	511.5	46.3	216	15	US-10-425-115-224762	Sequence 224762,
44	511.5	46.3	218	17	US-10-425-115-224759	Sequence 224759,
45	511	46.2	218	17		

ALIGNMENTS

RESULT 1

US-09-817-198A-2
Sequence 2, Application US/09817198A

Patent No. US20020146758A1

GENERAL INFORMATION:

APPLICANT: YE, Jane et al.

TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE

TITLE OF INVENTION: PROTEINS, AND USES THEREOF

FILE REFERENCE: CL001188

CURRENT APPLICATION NUMBER: US/09/817,198A

CURRENT FILING DATE: 2001-03-27

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 212

TYPE: PRT

ORGANISM: Human

US-09-817-198A-2

Query Match 100.0%; Score 1105; DB 9; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIKTVGKVKRIQ	60
Db	1	MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMKTIKTVGKVKRIQ	60
Qy	61	IWDTAGERYQTITKQYRRAQGIIFLVYDISSRSYOHIMKWSVDVDEYAPGVQKILIG	120
Db	61	IWDTAGERYQTITKQYRRAQGIIFLVYDISSRSYOHIMKWSVDVDEYAPGVQKILIG	120
Qy	121	NKADEQKRVGRQGOQLAKEYGMDFYTSACTNLNIKESFTLTLVLQHRKELEGL	180
Db	121	NKADEQKRVGRQGOQLAKEYGMDFYTSACTNLNIKESFTLTLVLQHRKELEGL	180

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QY 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212
Db 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212

RESULT 2
US-10-363-616-319
; Sequence 319, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 319
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-319

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Best Local Similarity 100.0%; Pred. No. 4.1e-100;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKQYDVLFRLLIGDSGVGKTCCLCRFTDNEFHSHSHSTIGVDFKMTIEVDGKVRQ 60
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QY 61 IWDTAGQERYQTITKQYRRAGQIFLVYDISSERSYQHIMKWSDVDVEYAPGVQKILIG 120
Db 61 IWDTAGQERYQTITKQYRRAGQIFLVYDISSERSYQHIMKWSDVDVEYAPGVQKILIG 120

QY 121 NKADBEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTRLTELVLQAHKLEGL 180
Db 121 NKADBEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTRLTELVLQAHKLEGL 180

QY 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212
Db 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212

RESULT 3
US-09-764-868-701
; Sequence 701, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PAM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 701
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-701

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Best Local Similarity 100.0%; Pred. No. 9.8e-100;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKQYDVLFRLLIGDSGVGKTCCLCRFTDNEFHSHSHSTIGVDFKMTIEVDGKVRQ 60
Db 27 MAKQYDVLFRLLIGDSGVGKTCCLCRFTDNEFHSHSHSTIGVDFKMTIEVDGKVRQ 86
QY 61 IWDTAGQERYQTITKQYRRAGQIFLVYDISSERSYQHIMKWSDVDVEYAPGVQKILIG 120

QY 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212
Db 181 RMRASNELALAELEEEGKPEGPNSSKTCWC 212

RESULT 4
US-09-817-198A-5
; Sequence 5, Application US/09817198A
; Patent No. US20020146758A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001188
; CURRENT APPLICATION NUMBER: US/09/817,198A
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Human
US-09-817-198A-5

Query Match 98.8%; Score 1092; DB 9; Length 218;
Best Local Similarity 97.2%; Pred. No. 8.1e-99;
Matches 212; Conservative 0; Mismatches 0; Indels 6; Gaps 1;

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QY 61 IWDTAGQERYQTITKQYRRAGQIFLVYDISSERSYQHIMKWSDVDVEYAPGVQKILIG 120
Db 61 IWDTAGQERYQTITKQYRRAGQIFLVYDISSERSYQHIMKWSDVDVEYAPGVQKILIG 120

QY 121 NKADBEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTRLTELVLQAHK 174
Db 121 NKADBEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTRLTELVLQAHK 180

QY 175 KELEGLRMRASNELALAELEEEGKPEGPNSSKTCWC 212
Db 181 KELEGLRMRASNELALAELEEEGKPEGPNSSKTCWC 218

RESULT 5
US-09-817-198A-4
; Sequence 4, Application US/09817198A
; Patent No. US20020146758A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001188
; CURRENT APPLICATION NUMBER: US/09/817,198A
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-817-198A-4
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OM protein - protein search, using sw model

Run on: December 25, 2004, 05:19:28 ; Search time 132 seconds
(without alignments)
106.511 Million cell updates/sec

Title: US-09-817-198C-2

Perfect score: 1105

Sequence: 1 MAKQYDVLFRLLIGDSGVG.....LEEERKPEGPANSGKTCWC 212

Scoring table: BLOSUM62

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	518.5	46.9	198	2	US-08-531-525-51
6	518.5	46.9	198	2	US-08-718-270A-51
7	515.5	46.7	203	4	US-09-255-920A-12
8	503.5	45.6	207	2	US-08-531-525-35
9	503.5	45.6	207	2	US-08-718-270A-35
10	494.5	44.8	215	2	US-08-531-525-10
11	494.5	44.8	215	2	US-08-718-270A-10
12	488.5	44.2	194	2	US-08-531-525-34
13	488.5	44.2	194	2	US-08-718-270A-34
14	478.5	43.3	201	2	US-08-916-901-3
15	478.5	43.3	201	3	US-09-154-602-3
16	473	42.8	213	4	US-09-248-796A-20293
17	469	42.4	201	2	US-08-916-901-8
18	469	42.4	201	3	US-09-154-602-8
19	467	42.3	205	4	US-09-709-103-49
20	467	42.3	205	4	US-09-439-410A-49
21	463	41.9	202	2	US-08-531-525-14
22	463	41.9	202	2	US-08-718-270A-14
23	462	41.8	227	4	US-09-248-796A-20291
24	453.5	41.0	201	2	US-08-531-525-13
25	453.5	41.0	201	2	US-08-718-270A-13
26	452.5	41.0	190	2	US-08-824-873-3
27	452.5	41.0	190	3	US-09-198-184-3

28	452.5	41.0	190	4	US-09-255-920A-7	Sequence 7, Appli
29	443	40.1	218	2	US-08-531-525-19	Sequence 19, Appl
30	443	40.1	218	2	US-08-718-270A-19	Sequence 19, Appl
31	438.5	39.7	227	4	US-09-270-767-46812	Sequence 46812, A
32	430.5	39.0	217	4	US-09-255-920A-15	Sequence 15, Appl
33	430	38.9	202	4	US-09-255-920A-11	Sequence 11, Appl
34	430	38.9	216	4	US-09-255-920A-14	Sequence 14, Appl
35	428	38.7	128	4	US-09-513-999C-5775	Sequence 5775, Ap
36	424	38.4	214	4	US-09-270-767-33012	Sequence 33012, A
37	424	38.4	214	4	US-09-270-767-48229	Sequence 48229, A
38	418	37.8	275	4	US-09-270-767-43635	Sequence 43635, A
39	416	37.6	191	3	US-09-075-454-3	Sequence 3, Appli
40	412.5	37.3	212	3	US-09-399-913-67	Sequence 67, Appl
41	412.5	37.3	212	4	US-09-350-614-67	Sequence 67, Appl
42	409.5	37.1	190	2	US-08-824-873-1	Sequence 1, Appli
43	409.5	37.1	190	3	US-09-198-184-1	Sequence 1, Appli
44	409.5	37.1	212	2	US-08-531-525-18	Sequence 18, Appl
45	409.5	37.1	212	2	US-08-718-270A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-824-873-4
; Sequence 4, Application US/08824873
; Patent No. 5843717
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl
; TITLE OF INVENTION: NOVEL RAB PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,873
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0240 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 207 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 234746
US-08-824-873-4

Query Match 49.3%; Score 545; DB 2; Length 207;
Best Local Similarity 52.9%; Pred. No. 3e-52;
Matches 99; Conservative 45; Mismatches 43; Indels 0; Gaps 0;

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 25, 2004, 01:55:59 ; Search time 92 Seconds
(without alignments)
1325.863 Million cell updates/sec

Title: US-09-817-198c-2
Perfect score: 1105
Sequence: 1 MAKQYDVLFRLLIGDSGVG.....LBEERKPEGPANSKTCWC 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1105	100.0	212	1	RB15_HUMAN	P59190 homo sapien
2	1090	98.6	212	1	RB15_MOUSE	Q8k386 mus musculu
3	1077	97.5	212	1	RB15_RAT	P35289 rattus norv
4	872	78.9	212	2	Q6DI36	Q6di36 brachydanio
5	798	72.2	168	2	Q91YW0	Q91yw0 mus musculu
6	686	62.1	143	2	Q6P412	Q6p412 xenopus lae
7	686	62.1	143	2	A6H63736	A6h63736 xenopus l
8	53.5	51.0	200	2	Q7T384	Q7t384 brachydanio
9	557	50.4	211	2	Q7Y82	Q7y82 caenorhabdi
10	557	50.4	211	2	BAD07034	Bad07034 caenorhab
11	546.5	49.5	204	2	O15971	O15971 drosophila
12	545	49.3	207	1	RB8A_CANFA	P61007 canis famil
13	545	49.3	207	1	RB8A_HUMAN	P61006 homo sapien
14	545	49.3	207	2	RA35848	Aap35848 homo sapi
15	541	49.0	207	2	Q8VCF6	Q8vcf6 m cell line
16	539.5	48.8	210	2	RAB8_DISOM	P21128 brachyopge o
17	538.5	48.7	201	2	Q6DGV5	Q6dgv5 brachydanio
18	536	48.5	206	2	Q6DKL2	Q6dkl2 rattus norv
19	534.5	48.4	200	2	Q6PAW9	Q6paw9 xenopus lae
20	534.5	48.4	200	2	A6H60015	A6h60015 xenopus l
21	532	48.1	218	2	RB13_HUMAN	P51153 homo sapien
22	532	48.1	203	2	Q6PG66	Q6pg66 homo sapien
23	531.5	48.1	200	1	RB10_DISOM	P22127 discopyge o
24	530.5	48.0	200	1	RB10_CANFA	P24409 canis famil
25	530.5	48.0	200	1	RB10_HUMAN	P61026 homo sapien
26	530.5	48.0	200	1	R10_MOUSE	P61027 mus musculu
27	530.5	48.0	200	2	CAG33584	Cag33584 homo sapi
28	528.5	47.8	203	1	RB13_RAT	P35286 rattus norv
29	528.5	47.8	207	1	RB8B_HUMAN	Q2930 homo sapien
30	528.5	47.8	207	1	RB8B_MOUSE	P61028 mus musculu
31	528.5	47.8	207	1	RB8B_RAT	P70550 rattus norv

32	528.5	47.8	207	2	O18338	O18338 drosophila
33	528.5	47.8	207	2	BAD07038	Bad07038 drosophil
34	526	47.6	202	1	RB13_MOUSE	Q9dd03 mus musculu
35	526	47.6	206	1	RB8A_MOUSE	P55258 mus musculu
36	523.5	47.4	204	2	Q7QEG1	Q7qegi anopheles g
37	521	47.1	206	2	Q9HET4	Q9het4 aspergillus
38	520.5	47.1	299	2	Q7PUB2	Q7pub2 anopheles g
39	519	47.0	216	2	O24466	O24466 arabidopsis
40	518	46.9	205	2	Q7RVG3	Q7rvg3 neuropepoxa
41	518	46.9	214	2	Q40218	Q40218 lotus japon
42	518	46.9	215	2	Q7XHP7	Q7xhp7 oryza sativ
43	515.5	46.7	216	2	Q40215	Q40215 lotus japon
44	515	46.6	216	2	Q6L502	Q6l502 oryza sativ
45	515	46.6	216	2	Q9FJF1	Q9fjf1 arabidopsis

ALIGNMENTS

RESULT 1
RB15_HUMAN
ID RB15_HUMAN STANDARD; PRT; 212 AA.
AC P59190; Q86TX7; Q81W89;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ras-related protein Rab-15.
GN Name=RB15;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22459283; PubMed=12508121; DOI=10.1038/nature01348;
RA Heilig R., Eckenberg R., Petit J.-L., Fonknechten N., Da Silva C.,
RA Cattolico L., Levy M., Barbe V., De Berardinis V., Urte-Vidal A.,
RA Pelletier E., Vico V., Anthouard V., Rowen L., Madan A., Qin S.,
RA Sun H., Du H., Pepin K., Artiguenave F., Robert C., Cruaud C.,
RA Bruels T., Jaillon O., Friedlander L., Samson G., Brottier P.,
RA Cure S., Segrens B., Aniere F., Samain S., Crespeau H., Abbasi N.,
RA Alach N., Boscut D., Dickhoff R., Dors M., Dubois I., Friedman C.,
RA Gouyvenoux M., James R., Madan A., Mailey-Estrada E., Mangenot S.,
RA Martins N., Menard M., Oztas S., Ratcliffe A., Shaffer T., Trask B.,
RA Vacherie B., Bellemere C., Belser C., Besnard-Gonnet M.,
RA Bartol-Mavel D., Boucard M., Briez-Silla S., Combette S.,
RA Dufosse-Laurent V., Ferron C., Lechaplais C., Louesse C., Muselet D.,
RA Magdelenat G., Pateau E., Petit E., Sirvain-Trukiewicz P., Trybou A.,
RA Vega-Czarny N., Bataille E., Bluet E., Bordelais I., Dubois M.,
RA Dumont C., Guerin T., Haffray S., Hammadi R., Muanga J., Pellouin V.,
RA Robert D., Wunderle E., Gauguet G., Roy A., Sainte-Marthe L.,
RA Verdier J., Verdier-Discal C., Hillier L.W., Fulton L., McPherson J.,
RA Matsuda F., Wilson R., Scarpelli C., Gyapay G., Wincker P., Saurin W.,
RA Quetier F., Waterston R., Hood L., Weissbach J.,
RT "The DNA sequence and analysis of human chromosome 14."
RL Nature 421:601-607(2003).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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OM protein - protein search, using sw model

Run on: December 25, 2004, 05:09:38 ; Search time 78 Seconds
(without alignments)
261.512 Million cell updates/sec

Title: US-09-817-198c-2

Perfect score: 1105

Sequence: 1 MAKQYDVLFRLLIGDSGVG.....LREEGKPEGPANSSKTCWC 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1077	97.5	212	2 F42148	GTP-binding protei
2	559	50.6	224	2 T33855	hypothetical prote
3	545	49.3	207	2 B49647	GTP-binding protei
4	545	49.3	207	2 B36364	GTP-binding protei
5	532	48.1	203	2 A49647	GTP-binding protei
6	531.5	48.1	200	2 A38625	GTP-binding protei
7	530.5	48.0	200	2 D36364	GTP-binding protei
8	530	48.0	209	2 B38625	GTP-binding protei
9	526	47.6	206	2 I78851	GTP-binding protei
10	522.5	47.3	200	2 B42148	GTP-binding protei
11	519	47.0	216	2 T45901	GTP-binding protei
12	514	46.5	201	2 T28971	hypothetical prote
13	512	46.3	216	2 S33900	GTP-binding protei
14	512	46.3	216	2 T43378	GTP-binding protei
15	510	46.2	200	2 S12790	GTP-binding protei
16	509	46.1	215	2 T14565	GTP-binding protei
17	508.5	46.0	215	2 S57478	GTP-binding protei
18	508	46.0	216	2 J50640	GTP-binding protei
19	507.5	45.9	222	2 T14405	small GTP-binding
20	506	45.8	216	2 S57471	GTP-binding protei
21	505.5	45.7	217	2 S36365	GTP-binding protei
22	502.5	45.5	215	2 S57462	GTP-binding protei
23	501	45.3	203	2 S51495	GTP-binding protei
24	495.5	44.8	204	2 J57589	Sec4p homolog - ye
25	492.5	44.6	215	2 S57474	GTP-binding protei
26	483.5	43.8	208	2 A34716	GTP-binding protei
27	483	43.7	208	2 A38202	GTP-binding protei
28	482	43.6	203	2 S34253	GTP-binding protei
29	480	43.4	202	2 S38740	GTP-binding protei

RESULT 1

F42148

GTP-binding protein rab15 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: F42148

R:Elferink, L.A.; Anzai, K.; Scheller, R.H.

J. Biol. Chem. 267, 5768-5775, 1992

A:Title: rab15, a novel low molecular weight GTP-binding protein specifically expressed ;

A:Reference number: A42148; MUID:92210533; PMID:1313420

A:Accession: F42148

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-212 <ELE>

A:Cross-references: UNIPROT:P35289; GB:M83679; NID:G206536; PIDN:AAA1995.1; PID:G206537
A:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; lipoprotein; nucleotide binding; P-loop; prenylated cysteine
F:9-124/Domain: translation elongation factor Tu homology <ETU>
F:15-22/Region: nucleotide-binding motif A (P-loop)
F:121-124/Region: GTP-binding NKXD motif
F:210,212/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

Query Match 97.5%; Score 1077; DB 2; Length 212;

Best Local Similarity 97.6%; Pred. No. 1e-78;

Matches 207; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNBFHSSHISTIGVDFFQMKTIQVQKIRIQ 60

Db 1 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNBFHSSHISTIGVDFFQMKTIQVQKIRIQ 60

QY 61 IWDTAGQERYQITTKQYVRRAGIFLVYDIISSERSVOHIMKWSVDVDEYAPGVQKILIG 120

Db 61 IWDTAGQERYQITTKQYVRRAGIFLVYDIISSERSVOHIMKWSVDVDEYAPGVQKILIG 120

QY 121 NKADEQKQVQREGQOQLKEYGMDFYETSACTNINIKESFTRLTELVLQAHKLEGL 180

Db 121 NKADEQKQVQREGQOQLKEYGMDFYETSACTNINIKESFTRLTELVLQAHKLEGL 180

QY 181 RWRASNEALALEEBEKGPEGPANSSKTCWC 212

Db 181 RTCASNELALEEBDEGKTEGPANSSKTCWC 212

RESULT 2

T33855

hypothetical protein D1037.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-Jan-2000

C:Accession: T33855

R:Ledwith, J.; Biewald, T.

submitted to the EMBL Data Library, November 1998

A:Description: The sequence of C. elegans cosmid D1037.

A:Reference number: Z21424
A:Accession: T33855
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-224 <LED>
A:Cross-references: EMBL:AF106592; PIDN:AAC78494.1; GSPDB:GN00019; CESP:D1037.4
A:Experimental source: strain Bristol N2; clone D1037
C:Genetics:
A:Gene: CESP:D1037.4
A:Map position: 1
A:Introns: 10/3; 62/2; 82/3; 181/1
C:Superfamily: ras transforming protein; translation elongation factor Tu homology

Query Match 50.6%; Score 559; DB 2; Length 224;
Best Local Similarity 55.3%; Pred. No. 2.6e-36;
Matches 105; Conservative 42; Mismatches 39; Indels 4; Gaps 1;
QY 1 MAKQYDVLFRLLIGDSGVGKTCCLCRFTDNEFHSSHTIGVDFKMTIEVDGKVRIO 60
DB 1 MAKTYDYLKLLIGDSGVGKTCVLFPSDDSFNNSFTISTIGIDFKIRTIELDGKRIKQ 60
QY 61 IWDTAGQERYQTITTKQYRRAGQIFLVYDISSERSYOHIMKWSVDVDEYAPGQVKILIG 120
DB 61 IWDTAGQERFRTITTAAYRGAMGILVYDITNEKSFDPNIRNWRNIEEHASADVERMILG 120
QY 121 NKADBEOKRQVREGOGQOLAKKEYGMDVETSACTNLAIKESFTRLTELVLQAHKKEGLE 180
DB 121 NKCDVNDKRVSKERGEKALDYGIKFMETSAKANINVENAFTFLARDIKAKMDKKLEGN 180
QY 181 RMRASNE 187
DB 181 SPOGSNQ 187

RESULT 3
B49647
GTP-binding protein rab8 - human
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: B49647; S36817
R:Zahraoui, A.; Joberty, G.; Arpin, M.; Fontaine, J.J.; Hellio, R.; Tavitian, A.; Louvard
J. Cell Biol. 124, 101-115, 1994
A:Title: A small rab GTPase is distributed in cytoplasmic vesicles in non polarized cell
A:Reference number: A49647; MUID:94124602; PMID:8294494
A:Accession: B49647
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-207 <ZAH>
A:Cross-references: UNIPROT:P61006; EMBL:X56741; NID:G452317; PIDN:CAA40065.1; PID:G4523
R:Joberty, G.; Tavitian, A.; Zahraoui, A.
FEBS Lett. 330, 323-328, 1993
A:Title: Isoprenylation of Rab proteins possessing a C-terminal Caax motif.
A:Reference number: S36817; MUID:93387463; PMID:8375503
A:Accession: S36817
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 175-186 <JOB>
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop;
F:9-124/Domain: translation elongation factor Tu homology <STU>
F:15-22/Region: nucleotide-binding motif A (P-loop)
F:121-124/Region: nucleotide-binding motif A (P-loop)
F:151-153/Region: GTP-binding NKXD motif
F:204/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

Query Match 49.3%; Score 545; DB 2; Length 207;
Best Local Similarity 52.9%; Pred. No. 2.6e-36;
Matches 99; Conservative 45; Mismatches 43; Indels 0; Gaps 0;
QY 1 MAKQYDVLFRLLIGDSGVGKTCCLCRFTDNEFHSSHTIGVDFKMTIEVDGKVRIO 60
DB 1 MAKTYDYLKLLIGDSGVGKTCVLFPSDDSFNNSFTISTIGIDFKIRTIELDGKRIKQ 60

QY 61 IWDTAGQERYQTITTKQYRRAGQIFLVYDISSERSYOHIMKWSVDVDEYAPGQVKILIG 120
DB 61 IWDTAGQERFRTITTAAYRGAMGILVYDITNEKSFDPNIRNWRNIEEHASADVERMILG 120
QY 121 NKADBEOKRQVREGOGQOLAKKEYGMDVETSACTNLAIKESFTRLTELVLQAHKKEGLE 180
DB 121 NKCDVNDKRVSKERGEKALDYGIKFMETSAKANINVENAFTFLARDIKAKMDKKLEGN 180
QY 181 RMRASNE 187
DB 181 SPOGSNQ 187

RESULT 4
B36364
GTP-binding protein rab8 - dog
C:Species: Canis lupus familiaris (dog)
C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: B36364; S15604
R:Chavrier, P.; Vingron, M.; Sander, C.; Simons, K.; Zerial, M.
Mol. Cell. Biol. 10, 6578-6585, 1990
A:Title: Molecular cloning of YP1/SEC4-related cDNAs from an epithelial cell line.
A:Reference number: A36364; MUID:91061765; PMID:2123294
A:Accession: B36364
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-207 <CHA>
A:Cross-references: UNIPROT:P61007; GB:X56385; NID:G920; PIDN:CAB56776.1; PID:G6006436
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding; lipoprotein; membrane trafficking; nucleotide binding; P-loop; F:
F:9-124/Domain: translation elongation factor Tu homology <STU>
F:15-22/Region: nucleotide-binding motif A (P-loop)
F:121-124/Region: GTP-binding NKXD motif
F:151-153/Region: GTP-binding SAK/L motif
F:204/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

Query Match 49.3%; Score 545; DB 2; Length 207;
Best Local Similarity 52.9%; Pred. No. 2.6e-36;
Matches 99; Conservative 45; Mismatches 43; Indels 0; Gaps 0;
QY 1 MAKQYDVLFRLLIGDSGVGKTCCLCRFTDNEFHSSHTIGVDFKMTIEVDGKVRIO 60
DB 1 MAKTYDYLKLLIGDSGVGKTCVLFPSDDSFNNSFTISTIGIDFKIRTIELDGKRIKQ 60
QY 61 IWDTAGQERYQTITTKQYRRAGQIFLVYDISSERSYOHIMKWSVDVDEYAPGQVKILIG 120
DB 61 IWDTAGQERFRTITTAAYRGAMGILVYDITNEKSFDPNIRNWRNIEEHASADVERMILG 120
QY 121 NKADBEOKRQVREGOGQOLAKKEYGMDVETSACTNLAIKESFTRLTELVLQAHKKEGLE 180
DB 121 NKCDVNDKRVSKERGEKALDYGIKFMETSAKANINVENAFTFLARDIKAKMDKKLEGN 180
QY 181 RMRASNE 187
DB 181 SPOGSNQ 187

RESULT 5
A49647
GTP-binding protein Rab13 - human
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C:Accession: A49647
R:Zahraoui, A.; Joberty, G.; Arpin, M.; Fontaine, J.J.; Hellio, R.; Tavitian, A.; Louvard
J. Cell Biol. 124, 101-115, 1994
A:Title: A small rab GTPase is distributed in cytoplasmic vesicles in non polarized cells
A:Reference number: A49647; MUID:94124602; PMID:8294494
A:Accession: A49647
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-203 <ZAH>
A:Cross-references: UNIPROT:P51153; EMBL:X75593; NID:G452319; PIDN:CAA53266.1; PID:G45231;
C:Superfamily: ras transforming protein; translation elongation factor Tu homology

Result No.	Score	Query Match	Length	DB	ID	Description	
1	1105	100.0	212	5	ABP62882	Human pol	
2	1105	100.0	212	6	AAE29096	Human Ras	
3	1105	100.0	401	4	AAU17136	Novel sig	
4	1105	100.0	401	7	ADB93844	Human nov	
5	1092	98.8	218	3	AAAB41604	Human ORF	
6	1077	97.5	212	7	AAE58127	Rat Prote	
7	832	75.3	188	4	AAU17555	Novel sig	
8	832	75.3	188	7	ADB94263	Human nov	
9	573	51.9	208	7	ADJ71123	Human hea	
10	546.5	49.5	204	4	ABT70670	Drosophil	
11	545	49.3	207	7	AAE58121	Human Pro	
12	545	49.3	213	4	ABB11916	Human Rab	
13	540	48.9	221	5	ABP41333	Human ova	
14	532	48.1	203	7	ADB83429	Human Pro	
15	532	48.1	203	7	AAE58125	Human Pro	
16	532	48.1	246	3	AAE58196	Lung canc	
17	530.5	48.0	200	3	AAE09979	Human Rab	
18	530.5	48.0	200	3	AAE19165	Amino aci	
19	530.5	48.0	200	4	AAE95340	Human pro	
20	530.5	48.0	200	8	ADN05082	Antipsori	
21	530.5	48.0	218	3	AAE56993	Human pro	
22	529.5	47.9	218	4	ABG07266	Novel hum	
23	528.5	47.8	207	4	ABE71647	Drosophil	
24	528.5	47.8	207	4	AAE67154	Amino aci	
25	528.5	47.8	207	4	AAE92628	Human pro	

CC therapeutic treatment. Diseases that may be treated include wound healing
 CC and tissue repair, burns, central nervous system disorders (e.g.
 CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 212 AA;

Query Match 100.0%; Score 1105; DB 5; Length 212;
 Best Local Similarity 100.0%; Pred. No. 2e-108;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGKVRQ 60
 Db 1 MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGKVRQ 60
 QY 61 IWDTAGQERYQTITKQYRRAGGIFLVYDIISSERSYQHIMKWSDVDVEYAPGVQKILIG 120
 Db 61 IWDTAGQERYQTITKQYRRAGGIFLVYDIISSERSYQHIMKWSDVDVEYAPGVQKILIG 120
 QY 121 NKADDEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTLRLTELVLQAHKKELEGL 180
 Db 121 NKADDEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTLRLTELVLQAHKKELEGL 180
 QY 181 RMRASNELALAELEEEGKPEGPANSSKTCWC 212
 Db 181 RMRASNELALAELEEEGKPEGPANSSKTCWC 212

RESULT 2
 AA029096
 ID AA029096 standard; protein; 212 AA.

AC AA029096;

XX 24-FEB-2003 (first entry)

XX Human Ras-like protein.

XX Human; Ras-like protein; inflammation; cell proliferation; apoptosis;
 KW immunodeficiency; neurodegenerative; Alzheimer's disease; cirrhosis;
 KW Parkinson's disease; wasting disease; cachexia; myocardial infarction;
 KW osteoporosis; atherosclerosis; glomerulonephritis; Crohn's disease;
 KW irritable bowel syndrome; multiple sclerosis; osteoarthritis; allergy;
 KW pancreatitis; autoimmune thyroiditis; rheumatoid arthritis; osteopathic;
 KW Sjogren's syndrome; infection; transgenic; gene therapy; neutropenic; gout;
 KW neuroprotective; vasotropic; cytostatic; dermatological; nephrotropic;
 KW ophthalmological; tranquiliser; cancer; stroke; Grave's disease; AIDS;
 KW asthma; anaemia; drug screening.

XX Homo sapiens.

Key	Location/Qualifiers
Binding-site	15..22
Modified-site	/note="ATP/GTP binding site motif A"
Modified-site	18..23
Modified-site	/note="N-myristoylation site"
Modified-site	29..32
Modified-site	/note="Casein kinase II phosphorylation site"
Modified-site	92..94
Modified-site	/note="Protein kinase C phosphorylation site"
Modified-site	101..109
Modified-site	/note="Tyrosine kinase phosphorylation site"
Modified-site	104..107
Modified-site	/note="Casein kinase II phosphorylation site"
Modified-site	136..141
Modified-site	/note="N-myristoylation site"
Modified-site	205..208
Modified-site	/note="N-glycosylation site"
Modified-site	206..208

FT /note="Protein kinase C phosphorylation site"
 XX WO200277193-A2.

XX 03-OCT-2002.

XX 27-MAR-2002; 2002WO-US009328.

XX 27-MAR-2001; 2001US-00817198.

XX (PEKE) PE CORP.

XX Gan W, Ye J, Di Francesco V, Beasley EM;

XX WPI; 2003-018913/01.

XX N-PSDB; AAD47168, AAD47619.

XX New isolated human Ras-like protein polypeptide, useful for diagnosing,
 PT treating or preventing inflammation and disorders associated with cell
 PT proliferation and apoptosis, e.g. AIDS, cancer, allergies, anemia, asthma
 PT or stroke.

XX Claim 1; Page 74; 82pp; English.

XX The invention relates to human Ras-like protein and its corresponding
 CC nucleic acid. The Ras-like protein and DNA is useful in the development
 CC of human therapeutics and diagnostic compositions. They are useful in the
 CC diagnosis, prevention and treatment of inflammation and disorders
 CC associated with cell proliferation and apoptosis, e.g. AIDS and other
 CC infectious or genetic immunodeficiencies, neurodegenerative disease e.g.
 CC Alzheimer's disease, Parkinson's disease, wasting diseases e.g. cachexia,
 CC ischaemic injuries e.g. myocardial infarction, stroke or reperfusion
 CC injury, toxin-induced diseases such as alcohol-induced liver damage or
 CC cirrhosis, osteoporosis or cancer. They are also used to treat disorders
 CC associated with inflammation including allergies, atopic dermatitis,
 CC atherosclerosis, asthma, anaemia, Crohn's disease, diabetes mellitus,
 CC lupus erythematosus, multiple sclerosis, osteoarthritis, pancreatitis,
 CC autoimmune thyroiditis, rheumatoid arthritis, Sjogren's syndrome,
 CC uveitis, trauma, or viral, bacterial, fungal, parasitic, protozoal or
 CC helminthic infections. The antibodies of the invention are useful in
 CC pharmacogenomic analysis or for tissue typing. The transgenic animals are
 CC useful for studying the function of a Ras-like protein, and identifying
 CC and evaluating modulators of its activity. Ras-like protein is used in
 CC drug screening assays and its DNA is used in gene therapy. The present
 CC sequence is human Ras-like protein

XX Sequence 212 AA;

Query Match 100.0%; Score 1105; DB 6; Length 212;
 Best Local Similarity 100.0%; Pred. No. 2e-108;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGKVRQ	60
Db	1	MAKQYDVLFRLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGKVRQ	60
QY	61	IWDTAGQERYQTITKQYRRAGGIFLVYDIISSERSYQHIMKWSDVDVEYAPGVQKILIG	120
Db	61	IWDTAGQERYQTITKQYRRAGGIFLVYDIISSERSYQHIMKWSDVDVEYAPGVQKILIG	120
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Db	121	NKADDEQKRVGREGQQQLAKEYGMDFYETSACTNLNLIKESFTLRLTELVLQAHKKELEGL	180
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Db	181	RMRASNELALAELEEEGKPEGPANSSKTCWC	212

RESULT 3

AAU17136

ID AAU17136 standard; protein; 401 AA.

Query Match	100.0%;	Score 3257;	DB 9;	Length 3257;
Best Local-Similarity	100.0%;	Pred. No. 0;		
Best Global-Similarity	100.0%;	Mismatches 0;	Indels 0;	Gaps 0;

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181 AGATGAAGACCATAGAGGTAGACGGCATCAAAAGTCGGGATACAGATCTGGGACACTGCAG 240
241 GGCAGGAGATACACAGACCATCAAAAGCAGTACTATCGGGGGCCAGGGGATATTTT 300
241 GGCAGGAGATACACAGACCATCAAAAGCAGTACTATCGGGGGCCAGGGGATATTTT 300
301 TGGTCTATGACATTAAGCAGCGGCTTTACCAACATCATATGAAGTGGGTCAAGTACG 360
301 TGGTCTATGACATTAAGCAGCGGCTTTACCAACATCATATGAAGTGGGTCAAGTACG 360
361 TGGATGAGTACCAACAGAGCGCTTCCAGAGATCCTTATTGGGAATTAAGGCTGATGAG 420
361 TGGATGAGTACCAACAGAGCGCTTCCAGAGATCCTTATTGGGAATTAAGGCTGATGAG 420
421 AGCAGAAACGGCAGGTGGGAAGAGAGCAAGGCGACAGCTGGCGAAGAGTATGGCATGG 480
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481 ACTTCTATGAACAGTGCCTGCACCAACCTCAACATTTAAAGAGTCAATTCACGGGCTCTGA 540
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901 GCTGTTTCCCGACCAAGCCCTGTACGACCCCAACGATGTGCCGCAAGCACTGTCTC 960
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961 ACCATCCCGACCAACAGCAGCCCTGTGAGTCCAGGCACTTTAGCTGCTC 1020
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1141 CTTGCTGTGACAGCTCGCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
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1201 GCTCGTGGGAGGTTCCACCTTGGATCCAGGAAGAACCTCCACCTGCTCGTGGGTG 1260
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1261 GGCCAAAGGCTACAGGGTGTCTTTCTCTTCCCCACCCCACTGTCTCATGTGCCA 1320
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1321 TGGGCTTGCCTCCCGAGTACCTTGCAGAAAGTGGAGCATCAGAGTAGGAGGAAACAGCAA 1380
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1981 CTGTTCTCTTTGGCCTTTAAGACAAAGCGCTCATCTTGGCCCTTACCTCTGATAGGCTT 2040
1981 CTGTTCTCTTTGGCCTTTAAGACAAAGCGCTCATCTTGGCCCTTACCTCTGATAGGCTT 2040
2041 GAGGTTTGCACACACTGTGGTACAGGTGGAGGGAAGAGGAGGAGGAGGAGGAGGAGG 2100
2041 GAGGTTTGCACACACTGTGGTACAGGTGGAGGGAAGAGGAGGAGGAGGAGGAGGAGG 2100
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2161 TTTAAAGAGGAAACAAGTAATTTTACAGTTCTTCTGGGGTTCCTGCCACCGTCCCAAGG 2220
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2281 CAGCCAAACAAAGAACTGGGTGTGAGTATTATCACTAAGAACCAAAATCCAGGGCA 2340
2341 CTCATATGTGAAGGATAAGAACCTTCACTTCTTACTCTCTCCTCCTCCTCCTCCTCCTCCT 2400

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 18:57:48 ; Search time 256 Seconds
(without alignments)
9043.123 Million cell updates

Title: US-09-817-198C-1

Perfect score: 3257

Sequence: 1 tgccgctgccgcccag.....aaaaaaaaaaaaaaaaaaaa 3237

Scoring table: IDENTITY NUC

Gapop 10^{-1.0} , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	202.6	6.2	412	US-09-513-999C-1698	Sequence 1698, Ap
2	174.2	5.3	730	US-09-300-958A-16	Sequence 16, Appl
3	159.2	4.9	1799	US-09-774-528-36	Sequence 36, Appl
4	156.6	4.8	1340	US-08-824-873-2	Sequence 2, Appli
5	156.6	4.8	1340	US-09-198-184-2	Sequence 2, Appli
6	156	4.8	925	US-08-916-501-4	Sequence 4, Appli
7	156	4.8	925	US-09-154-602-4	Sequence 4, Appli
8	145.2	4.5	615	US-09-513-999C-1782	Sequence 1782, Ap
9	144.6	4.4	3936	US-09-919-173-49	Sequence 49, Appl
10	141	4.3	2552	US-09-270-767-15247	Sequence 15247, A
11	139	4.3	1053	US-09-270-767-12052	Sequence 12052, A
12	138	4.2	842	US-09-255-920A-6	Sequence 6, Appli
13	137	4.2	828	US-09-513-999C-2183	Sequence 2183, Ap
14	136.2	4.2	875	US-09-075-454-10	Sequence 10, Appl
15	136.2	4.2	1106	US-09-620-312D-959	Sequence 959, App
16	135.2	4.2	2612	US-09-484-970B-142	Sequence 142, App
17	133.4	4.1	1069	US-09-620-312D-646	Sequence 646, App
18	133	4.1	135	US-09-513-999C-16632	Sequence 16632, A
19	127.2	3.9	1090	US-09-799-451-914	Sequence 914, App
20	124.2	3.8	723	US-09-016-434-1422	Sequence 1422, Ap
21	123.6	3.8	1102	US-09-620-312D-828	Sequence 828, App
22	122.6	3.8	8137	US-09-566-921-7	Sequence 7, Appli
23	120.6	3.7	847	US-08-773-423-4	Sequence 4, Appli
24	119.6	3.7	684	US-09-248-796A-6188	Sequence 6188, Ap
25	118.4	3.6	928	US-09-270-767-14743	Sequence 14743, A
26	118	3.6	645	US-09-270-767-1383	Sequence 1383, Ap
27	118	3.6	645	US-09-270-767-16665	Sequence 16665, A

ALIGNMENTS

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RESULT 1
US-09-513-999C-1698
; Sequence 1698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1698
; LENGTH: 412

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Query Match	6.2%	Score 202.6;	DB 4;	Length 412;
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Qy	77	GCTGCTGATCGGGGACTCCGGGGTGGGCAAGACCTGCTGTCGTGCCGCTTCAACCGACAA	136
Db	61	GCTGCTGATCGGGGACTCGGGGGTGGGGAAGACCTGTCCTGTTCCGCTTCTTCGAGGA	120
Qy	137	CGAGTTTCCACTCCTCGCACATCTCCACCATCGGTGTTGACTTTTAAGATGAAAGACCATAGA	196
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Qy	197	GGTAGA CCGGCATCAAGTCCGGATACAGATCTGGGACACTCGAGGCAGAGAGATACCA	256
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QY 257 GACCATCAAAAGCAGTACTATCGCGCGGCCAGGGATATTTTGGTCTATGACATTAG 316
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241 GACGATCAAAAGCGCTACTACAGGGTGCAATGGGCATCATGCTGGTCTAGACATCAC 300
QY 317 CAGCGAGCGCTCTTACCAGCATCATGAAAGTGGGTCAAGTACGTCGGATGAGTACGCACC 376
Db |||||
301 CAACGAGAAGTCTCTTCGCAACATCCGGAACCTGGATTGCAACATTGAGGAGCAGCCCTC 360
QY 377 AGAAGCGCTCCAGAAAGATCTTATTTGGGAATAGGCTGATGAGGAGCAGAA 427
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361 TCGAGACGTGCAAAAGATGATACTTGGGAACAAGTGTGATGTGAATGACAA 411

RESULT 2

US-09-300-958A-16
; Sequence 16, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 730
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-300-958A-16

Query Match 5.3%; Score 174.2; DB 4; Length 730;
Best Local Similarity 56.7%; Pred. No. 2.5e-37;
Matches 342; Conservative 0; Mismatches 258; Indels 3; Gaps 1;
QY 7 CTGCCCCCGCGAGTTCCTCCCGCCCGCTGGCGCCCGCAGTCATGCGGAGCAGTACGATGTC 66
Db 44 CCGACCCCGCGCGCGCGCTCCGCCCCCGCGCCCGCCCGCCGCTGCGGAGTACGACACC 103
QY 67 TGTTCGGCTGCTGCTGATCGGGACTCCGGGTGGGCAAGACTGCTGCTGTCGCGGT 126
Db 104 TCTTCAAGCTGCTCATCATCGCGGACAGCGGTGTGGGCAAGAGCAGTCTTACTGTCGTT 163
QY 127 TCACCGACAAAGAGTTCCTCCTCGCACATCTCCACCATCGGTGTTGACTTTAAGATGA 186
Db 164 TTGCAGACACATTTCTCAGGAGCTATCATACAGATCGGAGTGGATTTCAGATCC 223
QY 187 AGACCATAGAGGTAGCGGCATCAAGTGGGATACAGATCTGGGACACTGCGAGGCGAGG 246
Db 224 GGACCGTGGAGATCAACGGGGAGAGGTGAAGCTGCAGATCTGGGACACAGCGGGCAGG 283
QY 247 AGAGATACCAAGACCATCAAAAGCAGTACTATCGCGGGCCAGGGGATATTTTGGTCT 306
Db 284 AGCGCTTCGCAACCATCTCCACGTATATCGGGGACCCACCGGGTCAATTTGGTTT 343
QY 307 ATGACATTAGCAGCGCGCTTTACCAAGCATCATGAAGTGGGTCAAGTGGGATG 366
Db 344 ACACGCTCACCAGTCCGAGTCTTTGTCAACGTCAAGCGTGGCTTCAGAAATCAACC 403
QY 367 AGTACCCAGCAGGCGTCCAGAGATCTTATTTGGGAATAGGCTGATGAGGAGCAGA 426
Db 404 AGAAC---TGTGATGATGTGTGCGGAATATATAGTGGGTAAATGAAGATGACGACCCCTGAGC 460
QY 427 AACGGCAGGTGGGAAGAGAGCAAGGCGAGCAGCTGGCGAAGGAGTATGCGATGGACTTCT 486

Db 461 GGAAGGTGGTGAGACGGAAGATGCCTACAAATTCGCGGGCAGATGGCATCCAGTTGT 520
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Db |||||
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RESULT 3

US-09-774-528-36
; Sequence 36, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 36
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (124)..(831)
US-09-774-528-36

Query Match 4.9%; Score 159.2; DB 4; Length 1799;
Best Local Similarity 59.5%; Pred. No. 5.4e-33;
Matches 288; Conservative 0; Mismatches 193; Indels 3; Gaps 1;
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QY 289 AGGGGATATTTTGGTCTATGACATTAGCAGCGAGCGCTCTTACCAGACATCATGAGT 348

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 18:57:23 ; Search time 9548 Seconds
(without alignments)
12430.269 Million cell updates/sec

Title: US-09-817-198c-1

Perfect score: 3257

Sequence: 1 tgcgcgcgtccgcgcgcag.....aaaaaaaaaaaaaaaaaaaaa 3257

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_est2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	883.4	27.1	955	5	BC397021
5	856	26.3	957	5	BQ937298
6	847.2	26.0	915	5	BC397020
7	840.2	25.8	908	5	BQ716774
8	837.8	25.7	918	5	BC326279
9	810.6	24.9	901	5	BQ220195
10	807.8	24.8	926	5	BC348287
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14	792.2	24.3	820	5	BQ845866
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24	743.6	22.8	793	6	CA411919

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27	723.6	22.2	730	5	BC331206	BC331206
28	722	22.2	732	4	BM045331	BM045331
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32	704.6	21.6	724	5	BC352668	BC352668
33	704.6	21.6	731	5	BC388608	BC388608
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36	695.2	21.3	703	5	BQ821168	BQ821168
37	689.8	21.2	845	4	BQ760915	BQ760915
38	689.4	21.2	887	4	BQ766350	BQ766350
39	687.2	21.1	935	5	BQ876547	BQ876547
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43	644.2	19.8	891	2	BQ188717	BQ188717
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ALIGNMENTS

RESULT 1

CNSLTI18T

LOCUS

DEFINITION

human full-length cDNA clone CS0DIO28YMI1 of Placenta of Homo sapiens (human).

ACCESSION

BC248046

KEYWORDS

HTC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 3151)

AUTHORS

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

TITLE

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

JOURNAL

Unpublished

REMARK

Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/

REFERENCE

2 (bases 1 to 3151)

AUTHORS

Genoscope.

TITLE

Submitted (30-JAN-2003) Genoscope - Centre National de Sequencage :

JOURNAL

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

Location/Qualifiers

1..3151

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/db_xref="taxon:9606"

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LKSHSRV"

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 18:50:08 ; Search time 1459 Seconds
(without alignments)

11718.550 Million cell updates/sec

Title: US-09-817-198C-1

Perfect score: 3257

Sequence: 1 tgcgcgtgcgcgcgcgcag.....aaaaaaaaaaaaaaaaaaaaa 3257

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: Geneseqn2001a.*
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7: Geneseqn2002bs.*
8: Geneseqn2003a.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3257	100.0	3257	8	AAD47168	Aad47168 Human Ras
2	2696.6	82.8	3240	4	AAK82285	Aak82285 Human Imm
3	2696.6	82.8	28770	8	AAD47169	Aad47169 Human Ras
4	1568.2	48.1	1666	3	AAC75813	Aac75813 Human ORF
5	1192.8	36.6	7924	6	ABK40069	Abk40069 Human che
6	1192.8	36.6	7924	6	ABL34138	Abi34138 Human imm
7	1160.8	35.6	7924	6	ABK40070	Abk40070 Human che
8	1160.8	35.6	7924	6	ABL34139	Abi34139 Human imm
9	1160.6	35.6	2021	4	AA527053	Aas27053 cDNA enco
10	1160.6	35.6	2021	10	ADB93231	Adb93231 Human cDN
11	1000.2	30.7	1054	6	ABQ93361	Abq93361 Human cDN
12	866.2	26.6	895	2	AAZ22400	Aaz22400 Human bla
13	633	19.4	676	10	ADF82748	Adf82748 Leukaemia
14	569	17.5	594	12	ACH74635	Ach74635 Human gen
15	534.2	16.4	566	4	AA527472	Aas27472 cDNA enco
16	534.2	16.4	566	10	ADB93650	Adb93650 Human cDN
17	477.4	14.7	481	6	ABK44752	Abk44752 cDNA enco
18	438.8	13.5	463	6	ABL66992	Abi66992 Thyroid c
19	424.4	13.0	458	9	ACH33636	Ach33636 Human end
20	383	11.8	410	10	ADF81379	Adf81379 Leukaemia
21	313.4	9.6	320	2	AAT25457	Aat25457 Human gen

22	307	9.4	313	6	ABL38341	Abi38341 Human col
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25	228.4	7.0	2411	6	ABO54410	Abq54410 Human ova
26	217.8	6.7	1161	4	AAH75182	Aah75182 Nucleotid
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40	209	6.4	1859	9	ADB12721	Adb12721 Human pol
41	203.2	6.2	991	10	ADB52880	Adb52880 Primary r
42	202.6	6.2	412	3	AAC01700	Aac01700 Human sec
43	200.2	6.1	716	3	AAA40104	Aaa40104 Human Rab
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45	198.4	6.1	956	3	AAA96887	Aaa96887 Nucleotid

ALIGNMENTS

RESULT 1						
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ID	AAAD47168 standard; cDNA; 3257 BP.					
XX						
AC	AAAD47168;					
XX						
DT	24-FEB-2003 (first entry)					
XX						
DE	Human Ras-like protein encoding cDNA.					
XX						
KW	Human; Ras-like protein; inflammation; cell proliferation; apoptosis;					
KW	immunodeficiency; neurodegenerative; Alzheimer's disease; cirrhosis;					
KW	Parkinson's disease; wasting disease; cachexia; myocardial infarction;					
KW	osteoporosis; atherosclerosis; glomerulonephritis; Crohn's disease;					
KW	irritable bowel syndrome; multiple sclerosis; osteoarthritis; allergy;					
KW	pancreatitis; autoimmune thyroiditis; rheumatoid arthritis; osteopathic;					
KW	Sjogren's syndrome; infection; transgenic; gene therapy; neotropic; gout;					
KW	neuroprotective; vasotropic; cyostatic; dermatological; nephrotropic;					
KW	ophthalmological; tranquilliser; cancer; stroke; Grave's disease; AIDS;					
KW	asthma; anaemia; drug screening; gene; ss.					
XX						
OS	Homo sapiens.					
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PD	03-OCT-2002.					
XX						
PF	27-MAR-2002; 2002WO-US009328.					
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PR	27-MAR-2001; 2001US-00817198.					
XX						
PA	(PEKE) PE CORP.					
XX						
PI	Gan W, Ye J, Di Francesco V, Beasley EM;					
XX						

DR	WPI; 2003-018913/01.	Db	481	ACTTCTATGAACAAGTGGCTGCACCAACCTCAACATTAAAGAGTCAATTCAACGCTCTGA	540
DR	P-PSDB; AAE29096.	Qy	541	CAGAGCTGGTGTCTGCAGGGCCATAGGAAGAGCTGGAAGSCCTCCCGATGCGTGCAGCA	600
XX		Db	541	CAGAGCTGGTGTCTGCAGGGCCATAGGAAGAGCTGGAAGSCCTCCCGATGCGTGCAGCA	600
PT	New isolated human Ras-like protein polypeptide, useful for diagnosing,	Qy	601	ATGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGAGGCAAAACCCGAGGGCCACGCAAACT	660
PT	treating or preventing inflammation and disorders associated with cell	Db	601	ATGAGTTGGCACTGGCAGAGCTGGAGGAGGAGGAGGCAAAACCCGAGGGCCACGCAAACT	660
PT	proliferation and apoptosis, e.g. AIDS, cancer, allergies, anemia, asthma	Qy	661	CTTCGAAAACCTGGTGTCTGAGTCTGTGTGGGGACCCACACGACACCCCTTTTC	720
XX	or stroke.	Db	661	CTTCGAAAACCTGGTGTCTGAGTCTGTGTGGGGACCCACACGACACCCCTTTTC	720
PS	Claim 4; Page 73-74; 82pp; English.	Qy	721	CTCAGGAGGCCGTGGGCAGACAGAGGGAGCCGGGGCTTTGGCTGTGTCTCTCTCT	780
XX		Db	721	CTCAGGAGGCCGTGGGCAGACAGAGGGAGCCGGGGCTTTGGCTGTGTCTCTCTCT	780
CC	The invention relates to human Ras-like protein and its corresponding	Qy	781	GTGATGACCTATTGAGTATCAGTAGCCACTACTCCCTGTGCTGGCCCTGAGAGCGGCT	840
CC	nucleic acid. The Ras-like protein and DNA is useful in the development	Db	781	GTGATGACCTATTGAGTATCAGTAGCCACTACTCCCTGTGCTGGCCCTGAGAGCGGCT	840
CC	of human therapeutics and diagnostic compositions. They are useful in the	Qy	841	CTGCTGTATCTCAAGCAGCCCTCTGCCAGCCGCTCCACCTGGAGTGTCTTCTCA	900
CC	diagnosis, prevention and treatment of inflammation and disorders	Db	841	CTGCTGTATCTCAAGCAGCCCTCTGCCAGCCGCTCCACCTGGAGTGTCTTCTCA	900
CC	associated with cell proliferation and apoptosis, e.g. AIDS and other	Qy	901	GCCTGTTTCCCAGCCACAGAGCTGTCTACGACCCCCACGATGTGCCGAAAGCACTGTCTC	960
CC	Alzheimer's disease, Parkinson's disease, wasting diseases e.g. cachexia,	Db	901	GCCTGTTTCCCAGCCACAGAGCTGTCTACGACCCCCACGATGTGCCGAAAGCACTGTCTC	960
CC	ischaemic injuries e.g. myocardial infarction, stroke or reperfusion	Qy	961	ACCATCCCGCACCACAGACAGCAGCCGCTGAGTGCAGGCCACTTTTCAGTGTCTC	1020
CC	injury, toxin-induced diseases such as alcohol-induced liver damage or	Db	961	ACCATCCCGCACCACAGACAGCAGCCGCTGAGTGCAGGCCACTTTTCAGTGTCTC	1020
CC	cirrhosis, osteoporosis or cancer. They are also used to treat disorders	Qy	1021	CTTCTCCGTCATCGTGTCT	1080
CC	associated with inflammation including allergies, atopic dermatitis,	Db	1021	CTTCTCCGTCATCGTGTCT	1080
CC	atherosclerosis, asthma, anaemia, Crohn's disease, diabetes mellitus,	Qy	1081	TGACCCCTCCCTCCGCTGGTTCGTATCAAGTCTCTCAAAACCCGCTCCCTCTCTCTCTCT	1140
CC	lupus erythematosus, multiple sclerosis, gout, irritable bowel syndrome,	Db	1081	TGACCCCTCCCTCCGCTGGTTCGTATCAAGTCTCTCAAAACCCGCTCCCTCTCTCTCTCT	1140
CC	autoimmune thyroiditis, rheumatoid arthritis, Sjogren's syndrome,	Qy	1141	CCTGTGTGTGACGTGCT	1200
CC	uveitis, trauma, or viral, bacterial, fungal, parasitic, protozoal or	Db	1141	CCTGTGTGTGACGTGCT	1200
CC	helminthic infections. The antibodies of the invention are useful in	Qy	1201	GCTCGTGGGAGTTCACCCCTTGGATCCAGGAAGAACCCCTCCACCCCTGCTCTCTCTCTCT	1260
CC	pharmacogenomic analysis or for tissue typing. The transgenic animals are	Db	1201	GCTCGTGGGAGTTCACCCCTTGGATCCAGGAAGAACCCCTCCACCCCTGCTCTCTCTCTCT	1260
CC	useful for studying the function of a Ras-like protein, and identifying	Qy	1261	GGCCAAAGGCTACAGGGTGTCT	1320
CC	and evaluating modulators of its activity. Ras-like protein is used in	Db	1261	GGCCAAAGGCTACAGGGTGTCT	1320
CC	drug screening assays and its DNA is used in gene therapy. The present	Qy	1321	TGGGCT	1380
CC	sequence is human Ras-like protein encoding cDNA	Db	1321	TGGGCT	1380
XX		Qy	1381	CCGGGAGTCTCTGAGCCTGGGGCTGCCCTTACTCTTACCCATTTCCCGACGAGAGCTTTG	1440
QX	Sequence 3257 BP; 793 A; 892 C; 870 G; 702 T; 0 U; 0 Other;	Db	1381	CCGGGAGTCTCTGAGCCTGGGGCTGCCCTTACTCTTACCCATTTCCCGACGAGAGCTTTG	1440
Query Match	100.0%; Score 3257; DB 8; Length 3257;	Qy	1441	CCCTTGTCTGGCTGCCGCTGCTCTTTTGGGAACTGAGCTCAGAGGAGAGTGTCTTCAG	1500
Best Local Similarity	100.0%; Pred. No. 0;	Db	1441	CCCTTGTCTGGCTGCCGCTGCTCTTTTGGGAACTGAGCTCAGAGGAGAGTGTCTTCAG	1500
Matches 3257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Qy	1501	AGAAGGAAACAAATGAGGGGTGGAGGATATAAAAGTCACTTCTTCTTCTTCTTCTTCTTCTT	1560
Qy	1 TGGCCGCTGTCGCCCGCAGTTCCTCCGCCCCGCTGGCCCCAGTCATGGCGAAGCAGTAGC	Db	1501	AGAAGGAAACAAATGAGGGGTGGAGGATATAAAAGTCACTTCTTCTTCTTCTTCTTCTTCTT	1560
Db	1 TGGCCGCTGTCGCCCGCAGTTCCTCCGCCCCGCTGGCCCCAGTCATGGCGAAGCAGTAGC	Qy	1561	TGCAGCATGAACAATTTCTCTCCACCTGGCTCCCAATTTTAAAGATGTGGACCAAGGC	1620
Qy	61 ATGTGCTTTCGGGCTGTCTGATCGGGACTCCGGGATCGGGATGAGACCTGCTGCTGT	Db	1561	TGCAGCATGAACAATTTCTCTCCACCTGGCTCCCAATTTTAAAGATGTGGACCAAGGC	1620
Db	61 ATGTGCTTTCGGGCTGTCTGATCGGGACTCCGGGATCGGGATGAGACCTGCTGCTGT	Qy			
Qy	121 GCGCTTTCACCGACACGAGTTCCTCTCGCACATCTCCACCATCGGTGTGACTTTA	Db			
Db	121 GCGCTTTCACCGACACGAGTTCCTCTCGCACATCTCCACCATCGGTGTGACTTTA	Qy			
Qy	181 AGATGAAGACCATAGAGGTAGACGGCATCAAAAGTGGGATACAGATCTGGGACACTGCAG	Db			
Db	181 AGATGAAGACCATAGAGGTAGACGGCATCAAAAGTGGGATACAGATCTGGGACACTGCAG	Qy			
Qy	241 GCGAGAGAGATACCGACCATCAAAAGTATATCGGGGCCCGGAGGATATTTT	Db			
Db	241 GCGAGAGAGATACCGACCATCAAAAGTATATCGGGGCCCGGAGGATATTTT	Qy			
Qy	301 TGGTCTATGACATTTAGCAGCGGCTCTTACACGACATCATGAAGTGGGTCAAGTACG	Db			
Db	301 TGGTCTATGACATTTAGCAGCGGCTCTTACACGACATCATGAAGTGGGTCAAGTACG	Qy			
Qy	361 TGGATGAGTACCCACAGAGCGTCCAGAGATCTTTTGGGAATAAGGCTGATGAGG	Db			
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Qy	421 AGCAGAAAGCGAGTGGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	Db			
Db	421 AGCAGAAAGCGAGTGGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	Qy			
Qy	481 ACTTCTATGAACAAGTGGCTGCACCAACCTCAACATTAAAGAGTCAATTCAACGCTCTGA	Db			

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 24, 2004, 18:56:50 ; Search time 13354 Seconds
(without alignments)
11533.814 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3030.2	93.0	3326	9 BC040679	BC040679 Homo sapi
2	2696.6	82.8	190517	9 CENS01DX4	AL139022 Human chr
3	1423.8	43.7	2210	9 HSM806937	BX640825 Homo sapi
4	1192.8	36.6	7924	6 AX347040	Sequence
5	1192.8	36.6	7924	6 AX348456	Sequence
c 6	1160.8	35.6	7924	6 AX347041	Sequence
c 7	1160.8	35.6	7924	6 AX348457	Sequence
8	1000.2	30.7	1054	6 AX399903	Sequence
9	866.2	26.6	895	6 BD205055	Human nuc
10	866.2	26.6	895	6 AX014147	Sequence
11	813	25.0	3139	10 BC027769	BC027769 Mus muscu
12	633	19.4	676	6 AX781147	PUBMED
13	577.6	17.7	945	10 RATRAB15X	M03679 Sprague-Daw
14	496	15.2	579	6 CO730386	Sequence
15	477.4	14.7	481	6 AX396088	Sequence
c 16	438.8	13.5	463	6 AX334820	Sequence
17	423.6	13.0	270654	2 AC096084	Sequence
18	416.4	12.8	2560	10 BC013790	BC013790 Mus muscu
19	383	11.8	410	6 AX779778	Sequence

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21	378.2	11.6	1980	5 BC075754	BC075754 Danio rer
22	338.2	10.4	2348	5 BC063736	BC063736 Xenopus l
23	307	9.4	313	6 AX341683	Sequence
24	234.2	7.2	2048	9 BC002977	BC002977 Homo sapi
25	234.2	7.2	2818	9 AK025165	AK025165 Homo sapi
26	230.6	7.1	624	9 CR536583	CR536583 Homo sapi
27	230.6	7.1	1980	9 SS3268	SS3268 Homo sapien
28	229	7.0	621	9 CR542274	CR542274 Homo sapi
29	229	7.0	624	9 AF498943	AF498943 Homo sapi
30	229	7.0	624	9 BT007184	BT007184 Homo sapi
31	229	7.0	624	12 BT008275	BT008275 Synthetic
32	229	7.0	660	9 HSMRAB8	X56741 H.sapiens m
33	229	7.0	1971	6 CQ726143	CQ726143 Sequence
34	227.4	7.0	638	10 SS3270	SS3270 MBL=RAS-rel
35	225.4	6.9	1400	10 BC071176	BC071176 Rattus no
36	224.2	6.9	1337	10 BC019990	BC019990 Mus muscu
37	222.6	6.8	760	4 CFRAB8	X56385 Canine rab8
38	222	6.8	1018	5 BX930100	BX930100 Gallus ga
39	221.4	6.8	563	5 BX934711	BX934711 Gallus ga
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41	217.8	6.7	624	6 AX236078	Sequence
42	217.8	6.7	1128	9 BC020654	BC020654 Homo sapi
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ALIGNMENTS

BC040679 3326 bp mRNA linear PRI 29-JUN-2004
Homo sapiens RAB15, member RAS oncogene family, mRNA (cDNA clone MGC:42319 IMAGE:4817835), complete cds.

ACCESSION BC040679

VERSION MGC

KEYWORDS MGC

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 3326)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahy, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalls, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 3326)

Strausberg, R.

Direct Submission

Submitted (29-NOV-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 On Sep 16, 2003 this sequence version replaced gi:26251822.
 Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
 Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
 Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
 Kim MacDonald, Anara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
 Teika Olson, Diana Palomquist, Anca Petrescu, Anna Liisa Prabh,
 Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skaleka,
 Duane Smalhus, Jeff Stott, Miranda Tsai, George Yang, Jacque
 Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: iRAK Plate: 70 Row: p Column: 2.

FEATURES

source

Location/Qualifiers
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CDS

Query Match 93.0%; Score 3030.2; DB 9; Length 3326;
 Best Local Similarity 95.8%; Pred. No. 0;
 Matches 3187; Conservative 0; Mismatches 8; Indels 132; Gaps 2;
 QY 41 AGTCATGGCGAAGCAGTACGATGCTGTTCGGCTGCTGATCGGGGATCCCGGGT 100
 DB 1 AGTCATGGCGAAGCAGTACGATGCTGTTCGGCTGCTGATCGGGGATCCCGGGT 60
 QY 101 GGGCAAGACCTGCTGCTGTCGGCTTACCGACACGAGTTCCACTCTCCGACATCTC 160
 DB 61 GGGCAAGACCTGCTGCTGTCGGCTTACCGACACGAGTTCCACTCTCCGACATCTC 120
 QY 161 CACCATCGGTGTGAATTTAAGATGAAGACCATAGAGGTAGCGGCATCAAAAGTGGGAT 220
 DB 121 CACCATCGGTGTGAATTTAAGATGAAGACCATAGAGGTAGCGGCATCAAAAGTGGGAT 180
 QY 221 ACAGATCTGGGACACTGCGAGGCGAGAGATACAGACCATCAAAAGTGTACTATCG 280
 DB 181 ACAGATCTGGGACACTGCGAGGCGAGAGATACAGACCATCAAAAGTGTACTATCG 240
 QY 281 GCGGGCCCGAGGGATATTTTGGTCTATGACATTTAGCAGCGAGCGCTTTACAGACAT 340
 DB 241 GCGGGCCCGAGGGATATTTTGGTCTATGACATTTAGCAGCGAGCGCTTTACAGACAT 300

ORIGIN

QY 341 CATGAAGTGGGTCAAGTACGCTGGATGA----- 367
 DB 301 CATGAAGTGGGTCAAGTACGCTGGATGAAGGTAGGAGATGCCACCTCACTGCCGGGTGTGG 360
 QY 368 ----- 367
 DB 361 AGAGGTGCTCACCGGGGAAGCAAGCGAGGCCAGATGGGAAGGCAAAATGCTTCCAG 420
 QY 368 -----GTACGACCAAGAGCGCTCCAG 389
 DB 421 GAAGCTTTGCCCTTCCACAGCCCTGGATGAAGACCTCTGTGTACGACCAAGAGCGCTCCAG 480
 QY 390 AGATCTTTATTTGGGAATTAAGCTGATAGGAGCAGAAAACCGCAGGTGGGAAGAGAGCAAA 449
 DB 481 AAGATCTTTATTTGGGAATTAAGCTGATAGGAGCAGAAAACCGCAGGTGGGAAGAGAGCAAA 540
 QY 450 GGGCAGCAGCTGGCGAAGGAGTATGGCATGGACTTCTATGAACAAGTGCCTGCACCAAC 509
 DB 541 GGGCAGCAGCTGGCGAAGGAGTATGGCATGGACTTCTATGAACAAGTGCCTGCACCAAC 600
 QY 510 CTCACATTTAAAGAGTCAATTCACGGCTCTGACAGAGCTGGTCTGCAGGCCCATAGGAAG 569
 DB 601 CTCACATTTAAAGAGTCAATTCACGGCTCTGACAGAGCTGGTCTGCAGGCCCATAGGAAG 560
 QY 570 GAGCTGGAAGGCTTCGGATGCGTGCAGCAATGATGGCACTGGCAGAGCTGGAGGAG 629
 DB 661 GAGCTGGAAGGCTTCGGATGCGTGCAGCAATGATGGCACTGGCAGAGCTGGAGGAG 720
 QY 630 GAGGAGGGCAAAACCGAGGGCCACGAACTCTTCGAAAACTCTGCTGGTGTGAGTCTCTG 689
 DB 721 GAGGAGGGCAAAACCGAGGGCCACGAACTCTTCGAAAACTCTGCTGGTGTGAGTCTCTG 780
 QY 690 TGTGGGGCACCCACACGACACCCCTCTTCCCTCAGGAGGCCCGCTGGGCGACACAGGGGAG 749
 DB 781 TGTGGGGCACCCACACGACACCCCTCTTCCCTCAGGAGGCCCGCTGGGCGACACAGGGGAG 840
 QY 750 CCGGGCTTTGCGCTGCTGCTCTCTCGTGTGATGACCTATTTAGTATCAGTAGCA 809
 DB 841 CCGGGCTTTGCGCTGCTGCTCTCTCGTGTGATGACCTATTTAGTATCAGTAGCA 900
 QY 810 CTACTCCCGCTCGCTGGCCCTGAGAGCGGCTCTGCTGTCATCTCAAGCAGCCCTGTCTCC 869
 DB 901 CTACTCCCGCTCGCTGGCCCTGAGAGCGGCTCTGCTGTCATCTCAAGCAGCCCTGTCTCC 960
 QY 870 CAGCCCGTCAACCTGAGTGGTCTTTCTTACGCTGTTTTTCCCGACCCACAGCCCTGTCTAC 929
 DB 961 CAGCCCGTCAACCTGAGTGGTCTTTCTTACGCTGTTTTTCCCGACCCACAGCCCTGTCTAC 1020
 QY 930 GACCCCGACGATGTGCGCAAGCACTGTCTCACCATCCGACCCACCCACAGCAACAGCCA 989
 DB 1021 GACCCCGACGATGTGCGCAAGCACTGTCTCACCATCCGACCCACCCACAGCAACAGCCA 1080
 QY 990 GGGCTGGAGTCCAGGCCCACTTTTCAAGCTGCTCTTTCTCCGTCGATCGTGTCTTCTCTG 1049
 DB 1081 GGGCTGGAGTCCAGGCCCACTTTTCAAGCTGCTCTTTCTCCGTCGATCGTGTCTTCTCTG 1140
 QY 1050 CTTTTTCTCTTCCCGCACTTCTCTTTCTGTGACCCCTCCCTCCCGTGGGTTTCTGAT 1109
 DB 1141 CTTTTTCTCTTCCCGCACTTCTCTTTCTGTGACCCCTCCCTCCCGTGGGTTTCTGAT 1200
 QY 1110 CAAAGCTCTCAAAACCCCGTCCCGCTGCTGTGCTGTGTGACAGCTCGCTCTTCTCTTC 1169
 DB 1201 C-AAGCTCTCAAAACCCCGTCCCGCTGCTGTGCTGTGTGACAGCTCGCTCTTCTCTTC 1259
 QY 1170 CTTCTTAAGTATCCAAAGGGATGGACCCAGGCTCGTGGGAGGTTCCACCCCTTGGATCC 1229
 DB 1260 CTTCTTAAGTATCCAAAGGGATGGACCCAGGCTCGTGGGAGGTTCCACCCCTTGGATCC 1319
 QY 1230 AGGAAGAACCTCCACCCCTCGTGGTGGGCGCAAGGCTACAGGGTCTCTTCTCTC 1289
 DB 1320 AGGAAGAACCTCCACCCCTCGTGGTGGGCGCAAGGCTACAGGGTCTCTTCTCTC 1379
 QY 1290 TTCCCCCACCCTCTGCTCTCATGTGCCATGGGCGCTGCTCCCCAGTACCTGCGAAA 1349